

1/18

SEQUENCE LISTING

<110> SODE, Koji

<120> Glucose dehydrogenase beta-subunit and DNA encoding the same

<130> G780-OP1551

<141> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

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<221> CDS

<222> (258)..(761)

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<221> CDS

<222> (764)..(2380)

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<222> (2386)..(2466)

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tacgaatggc tgacacattg aatggactat aaaaccattg tccgttccgg aatgtgcgcg 180
tacatttcag gtccgcgccg atttttgaga aatatcaagc gtggttttcc cgaatccggt 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc 290

Met His Asn Asp Asn Thr Pro His Ser Arg Arg

1

5

10

2/18

cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa	338
His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln	
15 20 25	
ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tgc ctg aca ttg	386
Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu	
30 35 40	
cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg	434
Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met	
45 50 55	
acg ctt tcc gaa tgc ctg acc ggc aag aaa ggg ctc agc cgc gtg atc	482
Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile	
60 65 70 75	
ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tgc ttc aag acg gcc	530
Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala	
80 85 90	
gac agc ctg ccg cag ctc gcc ggc gcg ctc gcg tcc ggt tgc ctg acg	578
Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr	
95 100 105	
ccg gaa cag gaa tgc ctc gca ctg acg atc ctc gag gcc tgg tat ctc	626
Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu	
110 115 120	
ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc	674
Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe	
125 130 135	
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Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys	
140 145 150 155	
ccc ggc ttc tgg gcc gac aaa ccg atc gag agg caa gcc tg atg gcc	769
Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala	
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gat acc gat acg caa aag gcc gac gtc gtc gtc gtt gga tgc ggt gtc	817
Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val	
175 180 185	
gcg ggc gcg atc gtc gcg cat cag ctc gcg atg gcg ggc aag gcg gtg	865
Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val	
190 195 200	
atc ctg ctc gaa gcg ggc ccg cgc atg ccg cgc tgg gaa atc gtc gag	913
Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu	
205 210 215	
cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg	961
Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro	
220 225 230	
tgc agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac	1009

3/18

Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn	Asp	Tyr	
235					240					245					250	
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Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile	Arg	Ala	
				255					260					265		
gtg	ggc	ggc	acg	acg	tgg	cac	tgg	gcc	gcg	tcg	gcg	tgg	cgc	ttc	att	1105
Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg	Phe	Ile	
			270					275					280			
ccg	aac	gac	ttc	aag	atg	aag	agc	gtg	tac	ggc	gtc	ggc	cgc	gac	tgg	1153
Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg	Asp	Trp	
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Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala	Glu	Glu	
	300					305					310					
gag	ctc	ggc	gtg	tgg	ggc	ccg	ggc	ccc	gag	gaa	gat	ctg	tac	tcg	ccg	1249
Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	Ser	Pro	
315				320					325					330		
cgc	aag	cag	ccg	tat	ccg	atg	ccg	ccg	ctg	ccg	ttg	tcg	ttc	aac	gag	1297
Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe	Asn	Glu	
			335					340					345			
cag	acc	atc	aag	acg	gcg	ctg	aac	aac	tac	gat	ccg	aag	ttc	cat	gtc	1345
Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe	His	Val	
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gtg	acc	gag	ccg	gtc	gcg	cgc	aac	agc	cgc	ccg	tac	gac	ggc	cgc	ccg	1393
Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly	Arg	Pro	
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act	tgt	tgc	ggc	aac	aac	aac	tgc	atg	ccg	atc	tgc	ccg	atc	ggc	gcg	1441
Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile	Gly	Ala	
	380					385					390					
atg	tac	aac	ggc	atc	gtg	cac	gtc	gag	aag	gcc	gaa	cgc	gcc	ggc	gcg	1489
Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala	Gly	Ala	
395				400				405					410			
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Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly	Pro	Asp	
			415					420					425			
aag	cgc	atc	gtc	gcg	gcg	ctc	tac	aag	gac	aag	acg	ggc	gcc	gag	cat	1585
Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala	Glu	His	
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cgc	gtc	gaa	ggc	aag	tat	ttc	gtg	ctc	gcc	gcg	aac	ggc	atc	gag	acg	1633
Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile	Glu	Thr	
		445				450					455					
ccg	aag	atc	ctg	ctg	atg	tcc	gcg	aac	cgc	gat	ttc	ccg	aac	ggc	gtc	1681
Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn	Gly	Val	

4/18

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Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly			
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acc ggc gtg tgc ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc			1777
Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly			
495	500	505	
ccg cag gag atg acg tgc ctg atc ggt ttc cgc gac ggt ccg ttc cgc			1825
Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg			
510	515	520	
gcg acc gaa gcg gcg aag aag atc cac ctg tgc aac ctg tgc cgc atc			1873
Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile			
525	530	535	
gac cag gag acg cag aag atc ttc aag gcc ggc aag ctg atg aag ccc			1921
Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro			
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gac gag ctg gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag			1969
Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln			
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ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg			2017
Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val			
575	580	585	
ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc			2065
Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile			
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acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc			2113
Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg			
605	610	615	
gag gtc tac gcg acc gcc gcg aag gtg ctg ggc ggc acg gac gtc gtg			2161
Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val			
620	625	630	
ttc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tgc acg atc			2209
Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile			
635	640	645	650
atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg			2257
Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr			
655	660	665	
ttc gac cat ccg aac ctg ttc att tgc agc agc gcg acg atg ccg acc			2305
Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met Pro Thr			
670	675	680	
gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctg gcg ctg cgg			2353
Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg			
685	690	695	

5/18

atg tgc gac acg ctg aag aag gaa gtc tgacc gtg cgg aaa tct act ctc 2403
 Met Ser Asp Thr Leu Lys Lys Glu Val Val Arg Lys Ser Thr Leu
 700 705 710
 act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg 2451
 Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala
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 gcc gat gcg gcc gat c 2467
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<211> 168

<212> PRT

<213> Burkholderia cepacia

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 35 40 45
 Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser
 50 55 60
 Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu
 65 70 75 80
 Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln
 85 90 95
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
 100 105 110
 Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn
 115 120 125
 Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp
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<212> PRT

<213> Burkholderia cepacia

6/18

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		20					25						30		
Ala	Val	Ile	Leu	Leu	Glu	Ala	Gly	Pro	Arg	Met	Pro	Arg	Trp	Glu	Ile
		35					40					45			
Val	Glu	Arg	Phe	Arg	Asn	Gln	Pro	Asp	Lys	Met	Asp	Phe	Met	Ala	Pro
	50					55					60				
Tyr	Pro	Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn
65					70					75					80
Asp	Tyr	Leu	Ile	Leu	Lys	Gly	Glu	His	Lys	Phe	Asn	Ser	Gln	Tyr	Ile
				85					90					95	
Arg	Ala	Val	Gly	Gly	Thr	Thr	Trp	His	Trp	Ala	Ala	Ser	Ala	Trp	Arg
			100					105					110		
Phe	Ile	Pro	Asn	Asp	Phe	Lys	Met	Lys	Ser	Val	Tyr	Gly	Val	Gly	Arg
		115					120					125			
Asp	Trp	Pro	Ile	Gln	Tyr	Asp	Asp	Leu	Glu	Pro	Tyr	Tyr	Gln	Arg	Ala
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Glu	Glu	Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr
145					150					155					160
Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe
			165						170					175	
Asn	Glu	Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe
			180					185					190		
His	Val	Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly
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Arg	Pro	Thr	Cys	Cys	Gly	Asn	Asn	Asn	Cys	Met	Pro	Ile	Cys	Pro	Ile
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Gly	Ala	Met	Tyr	Asn	Gly	Ile	Val	His	Val	Glu	Lys	Ala	Glu	Arg	Ala
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Gly	Ala	Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly
			245						250					255	
Pro	Asp	Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala
			260					265					270		
Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile
		275					280					285			
Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn
	290					295					300				
Gly	Val	Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His
305					310					315					320
Pro	Gly	Thr	Gly	Val	Ser	Phe	Tyr	Ala	Ser	Glu	Lys	Leu	Trp	Pro	Gly

7/18

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Arg	Gly	Pro	Gln	Glu	Met	Thr	Ser	Leu	Ile	Gly	Phe	Arg	Asp	Gly	Pro				
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Phe	Arg	Ala	Thr	Glu	Ala	Ala	Lys	Lys	Ile	His	Leu	Ser	Asn	Leu	Ser				
		355					360					365							
Arg	Ile	Asp	Gln	Glu	Thr	Gln	Lys	Ile	Phe	Lys	Ala	Gly	Lys	Leu	Met				
	370					375					380								
Lys	Pro	Asp	Glu	Leu	Asp	Ala	Gln	Ile	Arg	Asp	Arg	Ser	Ala	Arg	Tyr				
385					390				395						400				
Val	Gln	Phe	Asp	Cys	Phe	His	Glu	Ile	Leu	Pro	Gln	Pro	Glu	Asn	Arg				
			405				410						415						
Ile	Val	Pro	Ser	Lys	Thr	Ala	Thr	Asp	Ala	Ile	Gly	Ile	Pro	Arg	Pro				
		420					425						430						
Glu	Ile	Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His				
	435					440					445								
Thr	Arg	Glu	Val	Tyr	Ala	Thr	Ala	Ala	Lys	Val	Leu	Gly	Gly	Thr	Asp				
	450					455					460								
Val	Val	Phe	Asn	Asp	Glu	Phe	Ala	Pro	Asn	Asn	His	Ile	Thr	Gly	Ser				
465				470					475						480				
Thr	Ile	Met	Gly	Ala	Asp	Ala	Arg	Asp	Ser	Val	Val	Asp	Lys	Asp	Cys				
			485				490						495						
Arg	Thr	Phe	Asp	His	Pro	Asn	Leu	Phe	Ile	Ser	Ser	Ser	Ala	Thr	Met				
		500					505						510						
Pro	Thr	Val	Gly	Thr	Val	Asn	Val	Thr	Leu	Thr	Ile	Ala	Ala	Leu	Ala				
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<212> PRT

<213> Burkholderia cepacia

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<213> Artificial Sequence

8/18

<220>

<223> Description of Artificial Sequence: primer

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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27

<210> 8

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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31

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<211> 16

<212> PRT

9/18

<213> Burkholderia cepacia

<400> 9

Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala
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<211> 25

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:consensus

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<222> (6, 17, 18, 19, 22)

<223> Xaa=unknown

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<210> 11

<211> 2410

<212> DNA

<213> Burkholderia cepacia

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<221> CDS

<222> (673)..(1950)

<400> 11

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 agccgcgaag aagatccatc tgtcgaacat gtcccgcatc aaccaggaga cgcagaagat 180
 cttaaggcc ggcaaactga tgaagcacga ggagctcgac gcgcagatcc gcgaccgttc 240
 cgcgcgctac gtgcagttcg acigtctcca cgagattctg ccgcagcccg agaaccgcat 300
 cgtgccgagc aagacggcca ccgacgcgat cgggatcccg cgccccgaga tcacgtatgc 360
 gatcgacgat tacgtgaagc gcggcgccgt gcacacgcgc gaggtctacg cgacggccgc 420
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10/18

cacgggcgcg aggatcatgg gcgcggatgc acgcgactcg gtcgtcgaca aggactgccg 540
 cacgttcgac catccgaacc tgttcccttc gagcagctcg acgatgccga ccgtcgggtac 600
 ggigaacgtg acgctgacga tcgcggcgct cgcgctgcgg atgtcggaca cgctgaagaa 660
 ggaagtciga cc gtg cgg aaa tct act ctc acc ttc ctc ctc gcc ggc tgc 711
 Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys
 1 5 10
 ctc gcg ctg ccc ggc ctc gca cgc gcg gcc gat tgc gcc gat ccg gcg 759
 Leu Ala Leu Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala
 15 20 25
 cat gtc aag cgc ggc gaa tac ctc gcc gtc gcg ggc gac tgc atg gca 807
 His Val Lys Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala
 30 35 40 45
 tgc cac acc gcg aag ggc ggc aag ccg ttc gcg ggc ggc ctc ggc atg 855
 Cys His Thr Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met
 50 55 60
 ccg gtg ccg atg ctc ggc aag atc tat acg agc aac atc aca ccg gat 903
 Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp
 65 70 75
 ccc gat acc ggc atc ggc aac tgg acg ttc gag gac ttc gag cgc gcg 951
 Pro Asp Thr Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala
 80 85 90
 gtg cgg cac ggc gla tgc aag aac ggc gac aac ctg tac ccg gcg atg 999
 Val Arg His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met
 95 100 105
 ccg tac gtg tgc tac gcg aag atc aac gac gac gac gtg caa gcg ctg 1047
 Pro Tyr Val Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu
 110 115 120 125
 tac gcg tac ttc atg cac ggc gtc gaa ccg gtc aag cag gcg ccg ccg 1095
 Tyr Ala Tyr Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro
 130 135 140
 aag aac gag atc ccc gcg ctg ctg agc atg cgc tgg ccg ctg aag atc 1143
 Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile
 145 150 155
 tgg aac tgg ctg ttc ctg aag gac ggc gtg tac cag ccg aag ccc gag 1191
 Trp Asn Trp Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu
 160 165 170
 cag agc gcc gag tgg aac cgc ggc gcc tat ctc gtg cag ggc ctc gcg 1239
 Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala
 175 180 185
 cac tgc agc acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag 1287
 His Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys
 190 195 200 205
 tgc ctc gac gaa acg ggc ggc agc ttc ctg tgc ggc tgc gtg ctc gcg 1335

Ser	Leu	Asp	Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala			
				210					215					220				
ggc	tgg	gac	ggc	tac	aac	atc	acg	tcc	gac	ccg	aac	gcg	ggg	atc	ggc	1383		
Gly	Trp	Asp	Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly			
				225					230					235				
ggc	tgg	acg	cag	cag	cag	ctc	gtc	cag	tac	ctg	cgc	acc	ggc	agc	gtg	1431		
Gly	Trp	Thr	Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val			
				240					245					250				
ccg	ggc	ctc	gcg	cag	gcg	gcc	ggc	ccg	atg	gcc	gag	gcg	atc	gag	cac	1479		
Pro	Gly	Leu	Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His			
				255					260					265				
agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	ggc	ccg	atg	gcc	gag	1527		
Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu			
270					275					280					285			
gcg	atc	gag	cac	agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	cgc	1575		
Ala	Ile	Glu	His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg			
				290					295					300				
tcg	tcg	tgg	ggc	aag	ccg	gcc	gag	gat	ggc	ctg	aag	ctg	cgc	ggc	gtc	1623		
Ser	Ser	Trp	Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val			
				305					310					315				
gcg	ctc	gcg	tcg	tcg	ggc	atc	gat	ccg	gca	ccg	ctg	tat	ctc	ggc	aac	1671		
Ala	Leu	Ala	Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn			
				320					325					330				
tgc	gcg	acc	tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggt	tac	1719		
Cys	Ala	Thr	Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr			
				335					340					345				
tac	ccg	ccg	tig	ttc	cac	aac	tcg	acg	gtc	ggc	gcg	tcg	aat	ccg	acc	1767		
Tyr	Pro	Pro	Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr			
350					355					360					365			
aac	ctc	gtg	cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgc	aag	gcc	ggc	agc	1815		
Asn	Leu	Val	Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser			
				370					375					380				
gag	gac	gtc	ggg	atg	ccc	gcg	ttc	cgc	cac	gag	ctg	tcg	gat	gcg	cag	1863		
Glu	Asp	Val	Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln			
				385					390					395				
atc	gcc	gcg	ctg	acg	aac	tac	ctg	acg	ggg	cag	ttc	ggc	aat	ccg	gcc	1911		
Ile	Ala	Ala	Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala			
				400					405					410				
gcg	aag	gtg	acc	gag	cag	gac	gtc	gcg	aag	ctg	cgc	tga	aacgcggcac			1960		
Ala	Lys	Val	Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
				415					420					425				
gcggcgaggc	agggcaacaa	tagaaaagag	gaggagcaca	gcacatcggg	cgggccccga											2020		

12/18

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aatccggtgc ggcacgccc cgcatcgttt tcgttgatcg agaccatgac accgaaccaa 2140
ccgtttctcg cgtcccagcg cgaatgtctg ctgctgctgt cccgaatcct gctcgtgac 2200
ctgttcgtga tgttcggctg gaagaagatt atcgacttct ccggtacgat cgcgttcatt 2260
ggcagcgagg ggcgcggcg gccgatcatc tcggcggcga tctccgtcgt gatggagctc 2320
atcgtcggga ttgcgatcct cgtcggtttc cagacgcggc cgctcgcgct gtigtctgcg 2380
ctgtacacga tcggtaccgg catcatcggc 2410

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<210> 12
 <211> 425
 <212> PRT
 <213> Burkholderia cepacia

<400> 12

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1				5				10					15		
Pro	Gly	Leu	Ala	Arg	Ala	Ala	Asp	Ser	Ala	Asp	Pro	Ala	His	Val	Lys
			20					25					30		
Arg	Gly	Glu	Tyr	Leu	Ala	Val	Ala	Gly	Asp	Cys	Met	Ala	Cys	His	Thr
		35					40					45			
Ala	Lys	Gly	Gly	Lys	Pro	Phe	Ala	Gly	Gly	Leu	Gly	Met	Pro	Val	Pro
	50					55				60					
Met	Leu	Gly	Lys	Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr
	65				70					75				80	
Gly	Ile	Gly	Asn	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His
			85					90					95		
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val
			100					105				110			
Ser	Tyr	Ala	Lys	Ile	Asn	Asp	Asp	Asp	Val	Gln	Ala	Leu	Tyr	Ala	Tyr
	115					120				125					
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu
	130					135				140					
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp
	145				150					155				160	
Leu	Phe	Leu	Lys	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Pro	Glu	Gln	Ser	Ala
			165					170					175		
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser
		180						185				190			
Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
	195					200				205					
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp
	210				215					220					
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Gly	Trp	Thr
	225				230					235				240	

13/18

Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Leu
				245					250					255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	Ser	Phe	Ser
			260					265					270		
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu
		275					280					285			
His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	Ser	Ser	Trp
	290					295					300				
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305					310					315					320
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
				325					330					335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Pro
			340					345					350		
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr	Asn	Leu	Val
		355					360					365			
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser	Glu	Asp	Val
	370					375					380				
Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln	Ile	Ala	Ala
385					390					395					400
Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
			405						410					415	
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
			420					425							

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

tgcaccgtgc ggaaatctac tctcact

27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

14/18

<400> 14

acttcccttct tcagcgtgtc cgacatc

27

<210> 15

<211> 1441

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (121).. (1398)

<400> 15

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gctgacgata gccgcgctcg cgctgcggat gtcggacacg ctgaagaagg aagtcigacc 120
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
      1           5           10           15
ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag 216
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
           20           25           30
cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag 264
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
           35           40           45
atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
           50           55           60
gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
           65           70           75           80
ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cgg cac 408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
           85           90           95
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg 456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
           100           105           110
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac 504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
           115           120           125
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag 552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
           130           135           140

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15/18

atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg	600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp	
145 150 155 160	
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc	648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala	
165 170 175	
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc	696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser	
180 185 190	
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac	744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp	
195 200 205	
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtg ctc gcc ggc tgg gac	792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp	
210 215 220	
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg	840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr	
225 230 235 240	
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc	888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val	
245 250 255	
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg	936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser	
260 265 270	
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg	984
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr	
275 280 285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccg cgg tcg tcg tgg	1032
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp	
290 295 300	
ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg	1080
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala	
305 310 315 320	
tcg tcg ggc atc gat ccg gcg cgg ctg tat ctc ggc aac tgc gcg acg	1128
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr	
325 330 335	
tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg	1176
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser	
340 345 350	
ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg	1224
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val	
355 360 365	
cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc	1272

16/18

Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile
 370 375 380
 ggg atg ccc gct ttc cgc tac gat ctg aac gac gcg cag atc gcc gcg 1320
 Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala
 385 390 395 400
 ctg acg aac tac gtc acc gcg cag ttc ggc aat ccg gcg gcg aag gtg 1368
 Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val
 405 410 415
 acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca 1418
 Thr Glu Gln Asp Val Ala Lys Leu Arg
 420 425
 cggcgcaacc gataggacag gag 1441

<210> 16

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 16

Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
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 Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
 20 25 30
 Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
 35 40 45
 Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
 50 55 60
 Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
 65 70 75 80
 Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
 85 90 95
 Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
 100 105 110
 Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
 115 120 125
 Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
 130 135 140
 Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
 145 150 155 160
 Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala
 165 170 175
 Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
 180 185 190

17/18

Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
		195					200					205			
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ala	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp
	210					215					220				
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Ser	Trp	Thr
225					230					235					240
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val
				245					250					255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser
			260					265					270		
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr
		275					280					285			
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp
	290					295					300				
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305					310					315					320
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
				325					330					335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser
			340					345						350	
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val
		355					360					365			
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile
	370					375					380				
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala
385					390					395					400
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
				405					410					415	
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
			420					425							

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

<222> (2, 3)

<223> Xaa=unknown

18/18

<400> 17

Cys Xaa Xaa Cys His

1

5

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

catgccatgg cacacaacga caacact

27

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

cccaagcttg ggtcagactt ccttcttcag c

31